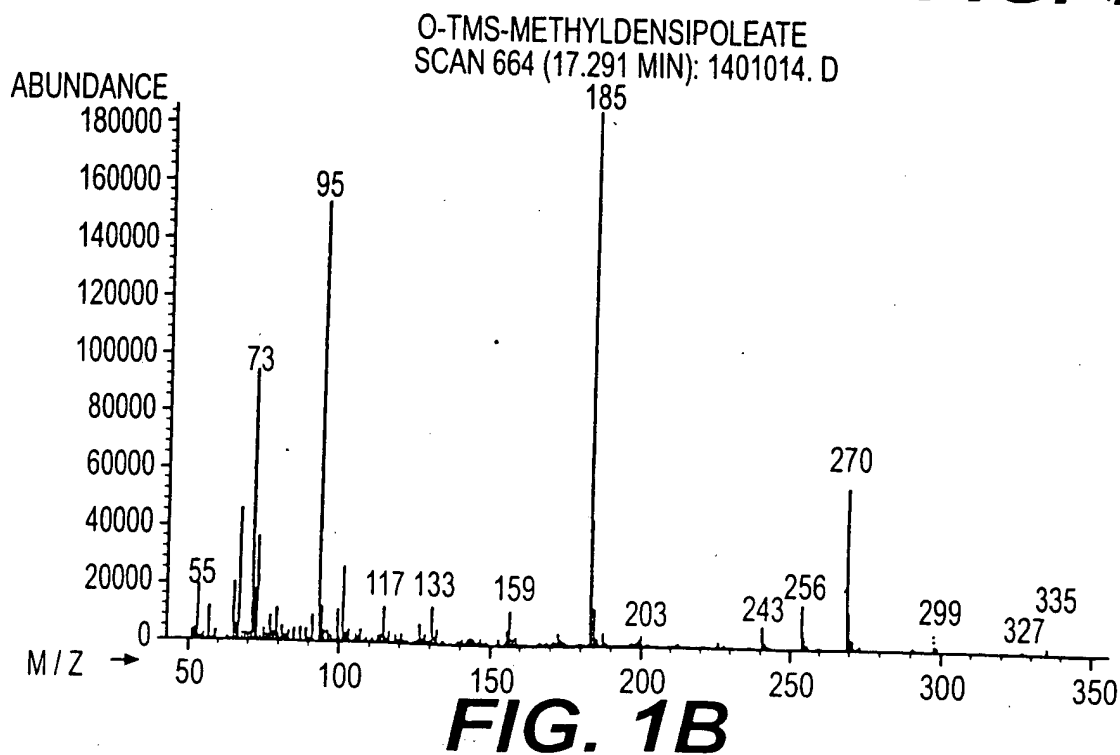


[illegible]

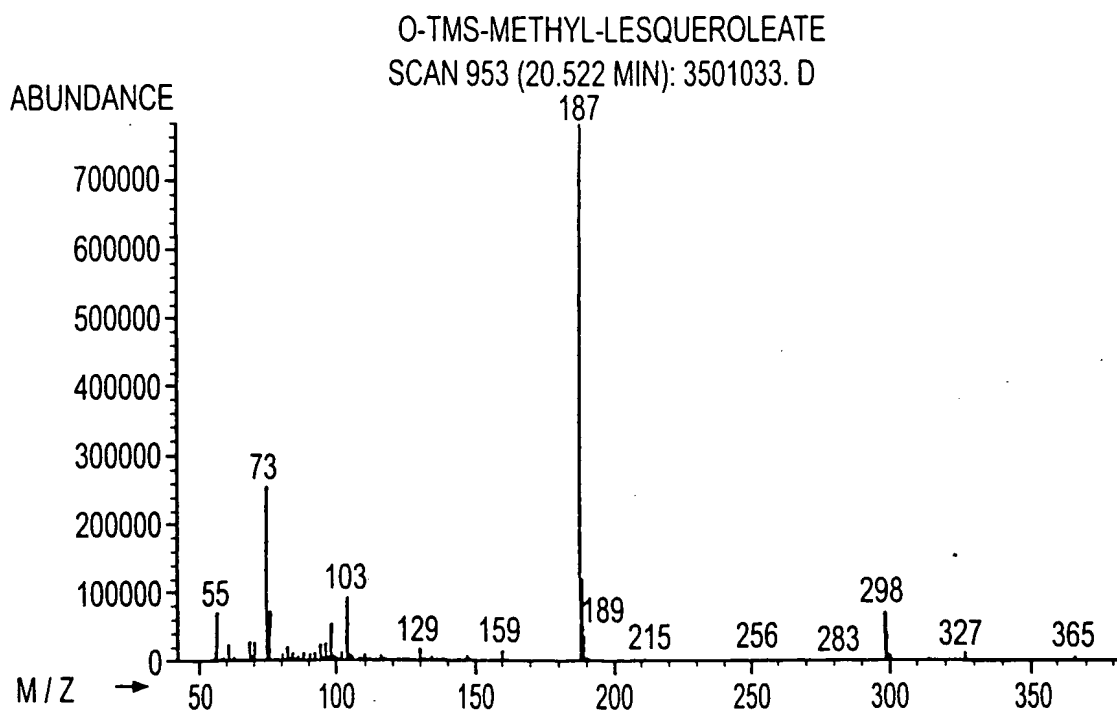


FIG. 1C

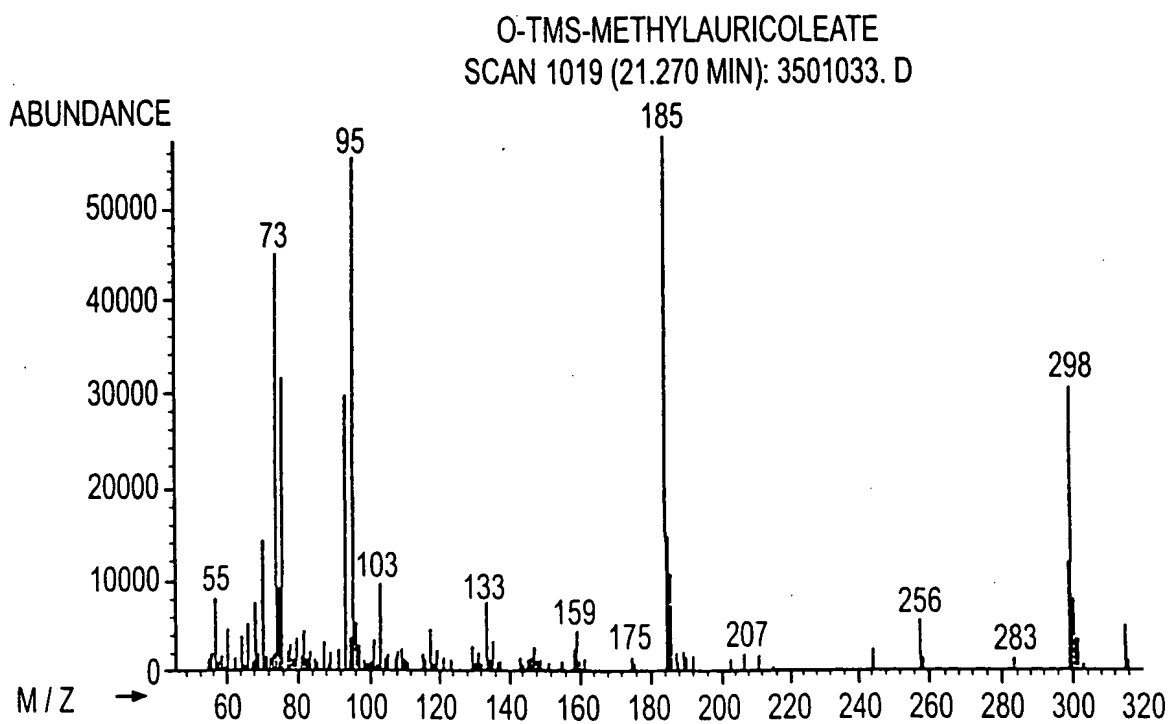
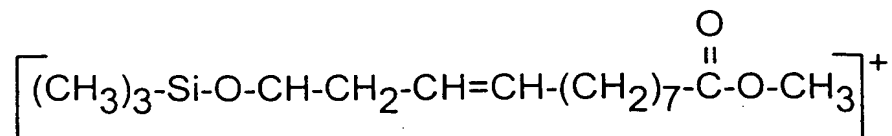


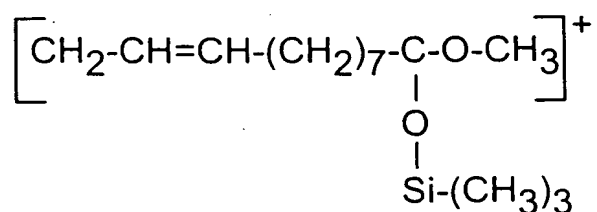
FIG. 1D

LON #1: MASS 187 $\left[\text{CH}_3-(\text{CH}_2)_5-\text{CH}-\text{O}-\text{Si}-(\text{CH}_3)_3 \right]^+$

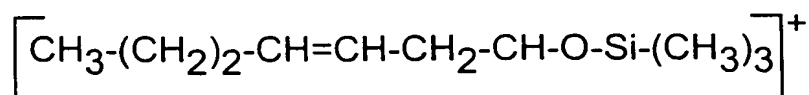
LON #2: MASS 299



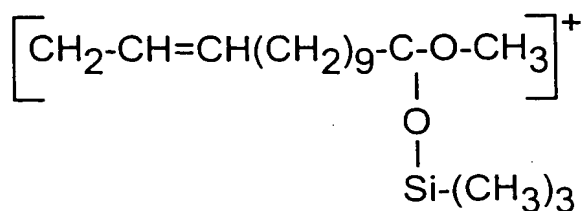
LON #3: MASS 270 (CHARACTERISTIC REARRANGEMENT ION)



LON #4: MASS 185 (DESATURATED ANALOG OF LON #1)



LON #5: MASS 298 (ELONGATED ANALOG OF LON #3)



LON #6: MASS 327 (ELONGATED ANALOG OF ION)

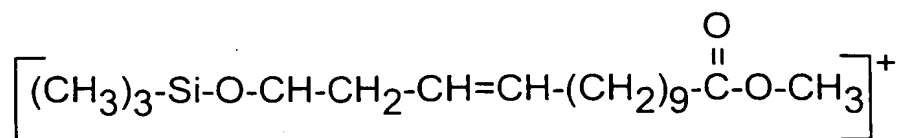


FIG. 2

FIG. 3A

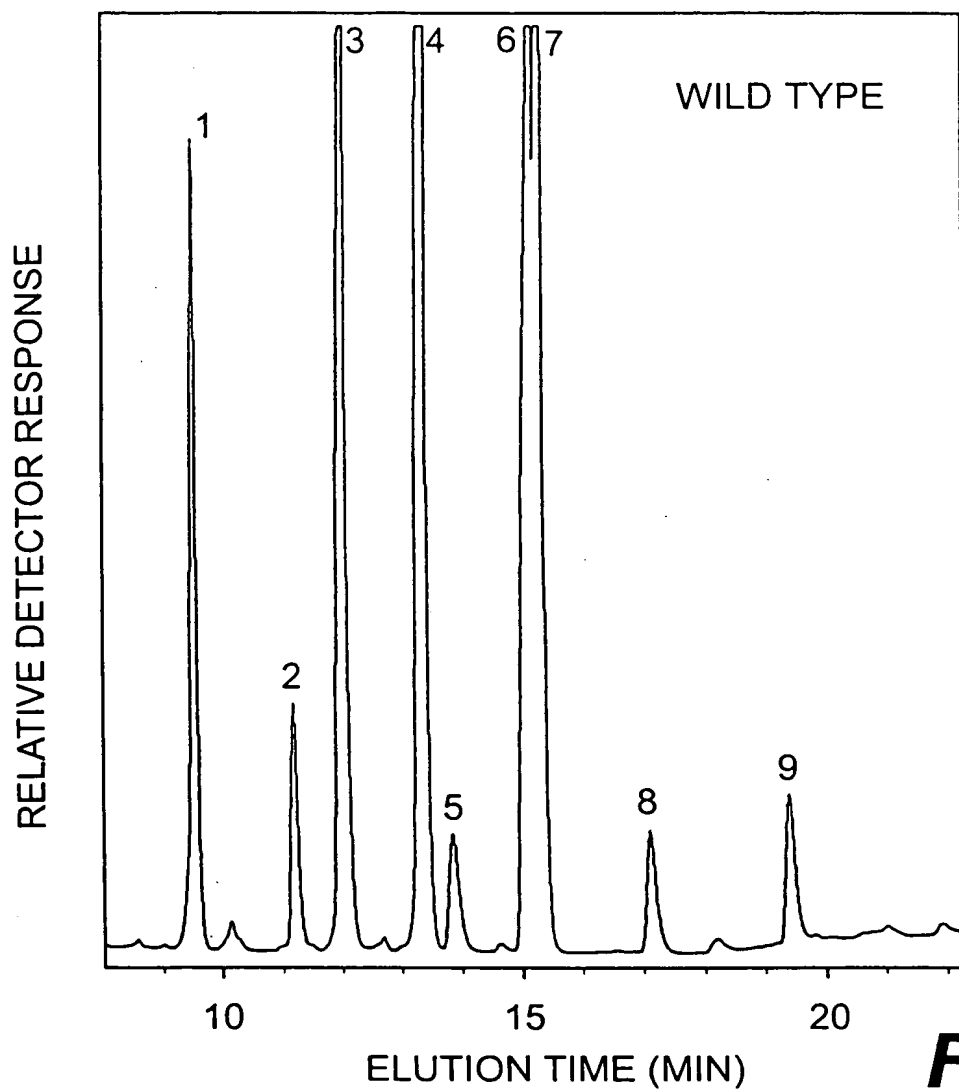


FIG. 3A

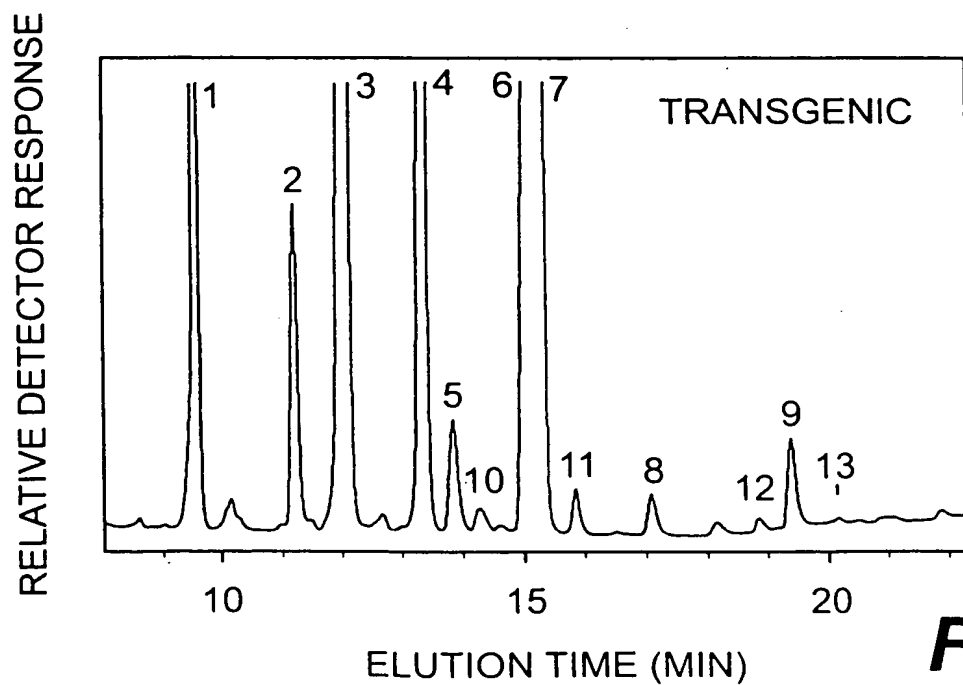


FIG. 3B

1501001.D

MASS SPECTRUM OF PEAK 10 FROM FIGURE 3B
SCAN 485 (15.203 MIN): 1501001.D

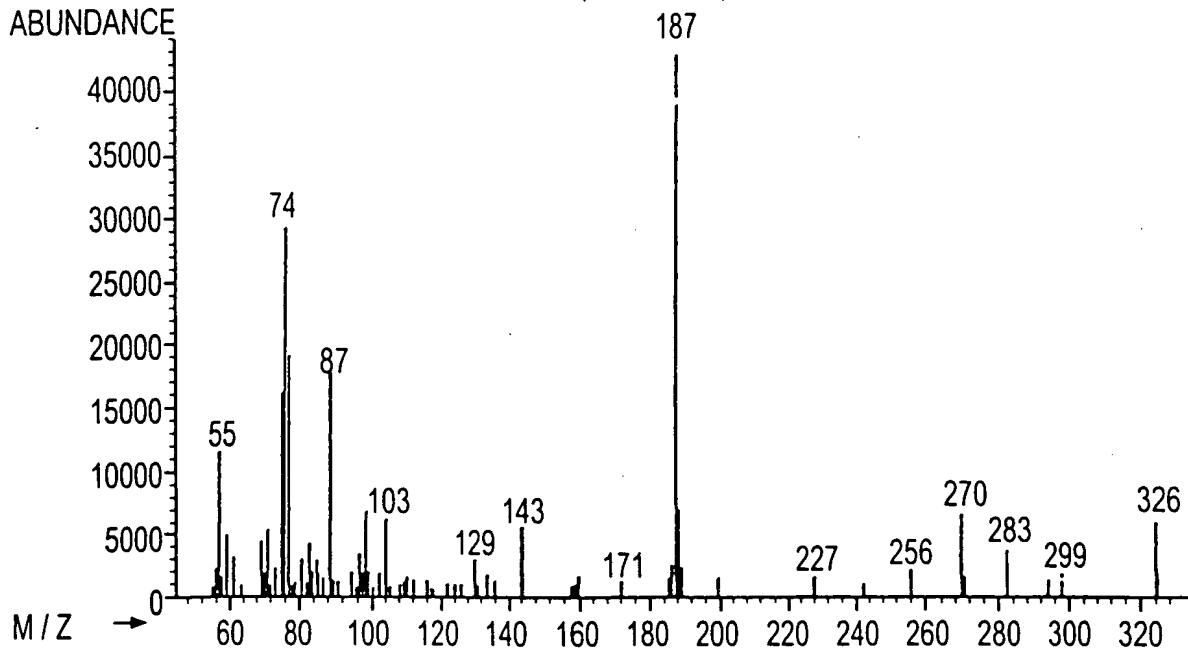


FIG. 4A

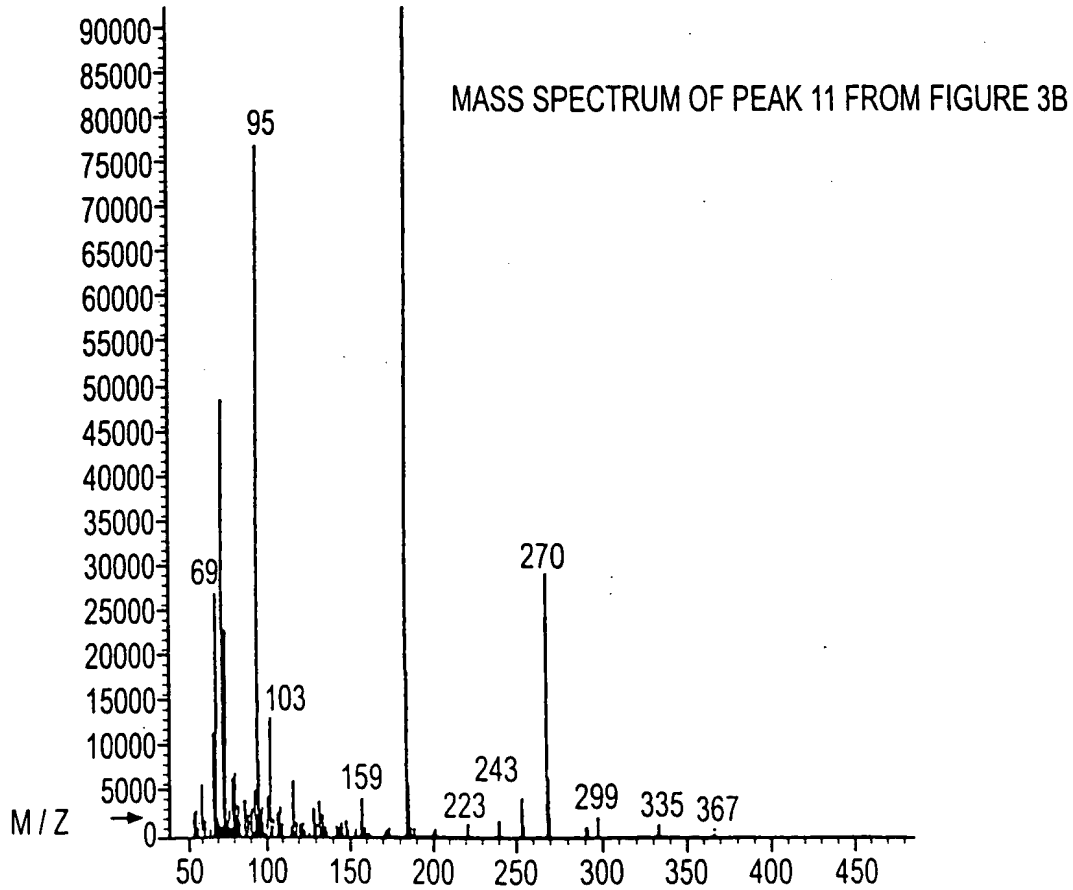


FIG. 4B

Mass spectrum of compound 10b. The x-axis represents the mass-to-charge ratio (m/z) from 50 to 350, and the y-axis represents relative abundance from 0 to 38000. The base peak is at m/z 187. Other labeled peaks include m/z 55, 73, 103, 129, 159, 186, 228, 256, 274, 298, 327, and 365.

MASS SPECTRUM OF PEAK 13 FROM FIGURE 3B
SCAN 997 (20.974 MIN): 1501001.D

ABUNDANCE

M/Z

M/Z	Relative Abundance (approx)
55	4000
75	25000
95	16000
117	3000
133	6000
159	3500
185	21000
203	2000
243	4500
256	7000
274	2500
298	5500
327	2500
371	2500

FIG. 4D

10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTT	CCTTGCTCTG	GTCACCTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

FIG. 5

10	20	30	40	50	60
TATAGCAC	GGAGGCACCA	TTCCAACACA	GGATCCCCTCG	AAAGAGATGA	AGTATTGTC
70	80	90	100	110	120
CCAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATG	TAACTGTCCA	GTTCTGCTCT	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTCTCTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCCTGCG
430	440	450	460	470	480
TTGCCCTCACT	ATGATTTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					
CACT					

FIG. 6

PROBE
PLesq3

PROBE
PLesq2

LEAF
SEED

SEED
LEAF

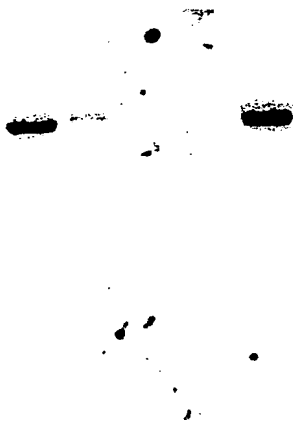


FIG. 7

AT	GAA	GCT	TTA	TAA	GAA	GTT	AGT	TTT	CTC	TGG	TGA	CAG	AGA	AAT	TNT	47
GCT	AAT	TGG	TAG	TGA	CAG	TTG	AAG	CAA	CAG	GAA	CAA	CAA	GGA	TGG	TTG	95
GTG	NTG	ATG	CTG	ATG	TGG	TGA	TGT	GTT	ATT	CAT	CAA	ATA	CTA	AAT	ACT	143
ACA	TTA	CTT	GTT	GCT	GCC	TAC	TTC	TCC	TAT	TTC	CTC	CGC	CAC	CCA	TTT	191
TGG	ACC	CAC	GAN	CCT	TCC	ATT	TAA	ACC	CTC	TCT	CGT	GCT	ATT	CAC	CAG	239
AAG	AGA	AGC	CAA	GAG	AGA	GAG	AGA	GAG	AAT	GTT	CTG	AGG	ATC	ATT	GTC	287
TTC	TTC	ATC	GTT	ATT	AAC	GTA	AGT	TTT	TTT	TGA	CCA	CTC	ATA	TCT	AAA	335
ATC	TAG	TAC	ATG	CAA	TAG	ATT	AAT	GAC	TGT	TCC	TTC	TTT	TGA	TAT	TTT	383
CAG	CTT	CTT	GAA	TTC	AAG	Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	10
						ATG	GGT	GCT	GGT	GGA	AGA	ATA	ATG	GTT	ACC	431
Pro	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	26
CCC	TCT	TCC	AAG	AAA	TCA	GAA	ACT	GAA	GCC	CTA	AAA	CGT	GGA	CCA	TGT	479
Glu	Lys	Pro	Pro	Phe	Thr	Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	42
GAG	AAA	CCA	CCA	TTC	ACT	GTT	AAA	GAT	CTG	AAG	AAA	GCA	ATC	CCA	CAG	527

FIG. 8A (CONT-1)

His CAT	Cys TGT	Phe TTC	Lys AAG	Arg CGC	Ser TCT	Ile ATC	Pro CCT	Arg CGT	Ser TCT	Phe TTC	Ser TCC	Tyr TAC	Leu CTT	Leu CTC	Thr ACA	58 575
Asp GAT	Ile ATC	Thr ACT	Leu TTA	Val GTT	Ser TCT	Cys TGC	Phe TTC	Tyr TAC	Tyr TAC	Val GTT	Ala GCC	Thr ACA	Asn AAT	Tyr TAC	Phe TTC	74 623
Ser TCT	Leu CTT	Leu CTT	Pro CCT	Gln CAG	Pro CCT	Leu CTC	Ser TCT	Thr ACT	Tyr TAC	Leu CTA	Ala GCT	Trp TGG	Pro CCT	Leu CTC	Tyr TAT	90 671
Trp TGG	Val GTA	Cys TGT	Gln CAA	Gly GGC	Cys TGT	Val GTC	Leu TTA	Thr ACC	Gly GGT	Ile ATC	Trp TGG	Val GTC	Ile ATT	Gly GGC	His CAT	106 719
Glu GAA	Cys TGT	Gly GGT	His CAC	His CAT	Ala GCA	Phe TTC	Ser AGT	Asp GAC	Tyr TAT	Gln CAA	Trp TGG	Val GTA	Asp GAT	Asp GAC	Thr ACT	122 767
Val GTT	Gly GGT	Phe TTT	Ile ATC	Phe TTC	His CAT	Ser TCC	Phe TTC	Leu CTT	Leu CTC	Val GTC	Pro CCT	Tyr TAC	Phe TTC	Ser TCC	Trp TGG	138 815
Lys AAA	Tyr TAC	Ser AGT	His CAT	Arg CGT	Arg CGT	His CAC	His CAT	Ser TCC	Asn AAC	Asn AAT	Gly GGA	Ser TCT	Leu CTC	Glu GAG	Lys AAA	154 863
Asp GAT	Glu GAA	Val GTC	Phe TTT	Val GTC	Pro CCA	Pro CCG	Lys AAG	Lys AAA	Ala GCT	Ala GCA	Val GTC	Lys AAA	Trp TGG	Tyr TAT	Val GTT	170 911
Lys AAA	Tyr TAC	Leu CTC	Asn AAC	Asn AAC	Pro CCT	Leu CTT	Gly GGA	Arg CGC	Ile ATT	Leu CTG	Val GTG	Leu TTA	Thr ACA	Val GTT	Gln CAG	186 959

FIG. 8A (CONT-2)

Phe TTT	Ile ATC	Leu CTC	Gly GGG	Trp TGG	Pro CCT	Leu TTG	Tyr TAT	Leu CTA	Ala GCC	Phe TTT	Asn AAT	Val GTA	Ser TCA	Gly GGT	Arg AGA	202 1007
Pro CCT	Tyr TAT	Asp GAT	Gly GGT	Phe TTC	Ala GCT	Ser TCA	His CAT	Phe TTC	Phe TTC	Pro CCT	His CAT	Ala GCA	Pro CCT	Ile ATC	Phe TTT	218 1055
Lys AAA	Asp GAC	Arg CGA	Glu GAA	Arg CGC	Leu CTC	Gln CAG	Ile ATA	Tyr TAC	Ile ATC	Ser TCA	Asp GAT	Ala GCT	Gly GGT	Ile ATT	Leu CTA	234 1103
Ala GCT	Val GTC	Cys TGT	Tyr TAT	Gly GGT	Leu CTT	Tyr TAC	Arg CGT	Tyr TAC	Ala GCT	Ala GCT	Ser TCA	Gln CAA	Gly GGA	Leu TTG	Thr ACT	250 1151
Ala GCT	Met ATG	Ile ATC	Cys TGC	Val GTC	Tyr TAT	Gly GGA	Val GTA	Pro CCG	Leu CTT	Leu TTG	Ile ATA	Val GTG	Asn AAC	Phe TTT	Phe TTC	266 1199
Leu CTT	Val GTC	Leu TTG	Val GTA	Thr ACT	Phe TTC	Leu TTG	Gln CAG	His CAC	Thr ACT	His CAT	Pro CCT	Ser TCG	Leu TTA	Pro CCT	His CAT	282 1247
Tyr TAT	Asp GAT	Ser TCA	Thr ACC	Glu GAG	Trp TGG	Glu GAA	Trp TGG	Ile ATT	Arg AGA	Gly GGA	Ala GCT	Leu TTG	Val GTT	Thr ACG	Val GTA	298 1295
Asp GAC	Arg AGA	Asp GAC	Tyr TAT	Gly GGA	Ile ATA	Leu TTG	Asn AAC	Lys AAG	Val GTG	Phe TTC	His CAT	Asn AAC	Ile ATA	Thr ACA	Asp GAC	314 1343
Thr ACA	His CAT	Val GTG	Ala GCT	His CAT	His CAT	Leu CTC	Phe TTT	Ala GCA	Thr ACT	Ile ATA	Pro CCG	His CAT	Tyr TAT	Asn AAC	Ala GCA	330 1391

FIG. 8B (CONT-1)

Met	Glu	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	346
ATG	GAA	GCT	ACA	GAG	GCG	ATA	AAG	CCA	ATA	CTT	GGT	GAT	TAC	TAC	CAC	1439
Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	362
TTC	GAT	GGA	ACA	CCG	TGG	TAT	GTG	GCC	ATG	TAT	AGG	GAA	GCA	AAG	GAG	1487
Cys	Leu	Tyr	Val	Glu	Pro	Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	378
TGT	CTC	TAT	GTA	GAA	CCG	GAT	ACG	GAA	CGT	GGG	AAG	AAA	GGT	GTC	TAC	1535
Tyr	Tyr	Asn	Asn	Lys	Leu											384
TAT	TAC	AAC	AAT	AAG	TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	1583
ATC	AAT	CTT	CAT	TTC	CAT	GTT	TTA	GGT	GTC	TTG	TTT	AAG	AAG	CTA	TGC	1631
TTT	GTT	TCA	ATA	ATC	TCA	GAG	TCC	ATN	TAG	TTG	TGT	TCT	GGT	GCA	TTT	1679
TGC	CTA	GTT	ATG	TGG	TGT	CGG	AAG	TTA	GTG	TTC	AAA	CTG	CTT	CCT	GCT	1727
GTG	CTG	CCC	AGT	GAA	GAA	CAA	GTT	TAC	GTG	TTT	AAA	ATA	CTC	GGA	ACG	1775
AAT	TGA	CCA	CAA	NAT	ATC	CAA	AAC	CGG	CTA	TCC	GAA	TTC	CAT	ATC	CGA	1823
AAA	CCG	GAT	ATC	CAA	ATT	TCC	AGA	GTA	CTT	AG						1855

FIG. 8B (CONT-2)

LFFAH12	1	10	MGAGGRIM--	--VTPSSKKS	20	--ETEALKRG	30	PCEKPPFTVK	40	50
FAH12	1		MGGGRMSTV	ITSNNSEKKG		--GSSHLKRA		PHTKPPFTLG		DLKRAIPPHC
ATFAD2	1		MGAGGRMP--	--VPTSSKKS		--ETDTTKRV		PCEKPPFSVG		DLKKAIPPHC
BNFAD2	1		MGAGGRMQ--	--VSPPSKKS		--ETDNIKRV		PCETPPFTVG		ELKKAIPPHC
GMFAD2-1	1		MGLA-KETTM	GGRGRVAKVE		VQKKKPLSRV		PNTKPPFTVG		QLKKAIPPHC
GMFAD2-2	1		MGAGGR----	TDVPPANRKS		--EVDPLKRV		PFEKPPQSLS		QIKKAIPPHC
ZMFAD2	1		MGAGGRMTEK	EREKQEQLAR		ATGGAAMQRS		PVEKPPFTLG		QIKKAIPPHC
RCFAD2	1		-----	-----		-----		-----		-----
		60		70	80			90	100	
LFFAH12	51		FKRSIPRSFS	YLLTDITLVS		CFYYVATNYF		SLLPQPLSTY		LAWPLYWVCQ
FAH12	51		FERSFVRFS	YVAYDVCLSF		LFYSIATNFF		PYISSPLS-Y		VAWL VYWL FQ
ATFAD2	51		FKRSIPRSFS	YLI SDII IAS		CFYYVATNYF		SLLPQPLS-Y		LAWPLYWACQ
BNFAD2	51		FKRSIPRSFS	HLIWDII IAS		CFYYVATTYF		PLLPNPLS-Y		FAWPLYWACQ
GMFAD2-1	51		FQSLTTSFS	YVVYDLSFAF		IFY-IATTYF		HLLPQPLS-L		IAWPIYWVLQ
GMFAD2-2	51		FQSVLRSFS	YVVYDLTIAF		CLYYVATHYF		HLLPGPLS-F		RGMAIYWAVQ
ZMFAD2	51		FERSVLKSFS	YVVHDLVIAA		ALLYFALAI I		PALPSPLR-Y		AAWPLYWIAQ
RCFAD2	1		-----	-----		-----		-----		-----
		110		120	130			140	150	
LFFAH12	101		GCVLTGIWVI	GHECGHHA FS		DYQWVDDTVG		FIFHSFLLVP		YFSWKYSHRR
FAH12	101		GCILTGLWVI	GHECGHHA FS		EYQLADDIVG		LIVHSALLVP		YFSWKYSHRR
ATFAD2	101		GCVLTGIWVI	AHECGHHA FS		DYQWLDDTVG		LIFHSFLLVP		YFSWKYSHRR
BNFAD2	101		GCVLTGVWVI	AHECGHHA FS		DYQWLDDTVG		LIFHSFLLVP		YFSWKYSHRR
GMFAD2-1	101		GCLLTGVWVI	AHECGHHA FS		KYQWVDDVVG		LTLSHSTLLVP		YFSWKISHRR
GMFAD2-2	101		GCILTGVWVI	AHECGHHA FS		DYQLLDDIVG		LILHSALLVP		YFSWKYSHRR
ZMFAD2	101		G-----	-----AFS		DYSLDDDVVG		LVLHSSLMVP		YFSWKYSHRR
RCFAD2	101		-----WVM	AHDCGHHA FS		DYQLLDDVVG		LILHSCLLVP		YFSWKHSHRR

FIG. 9A (CONT-1)

LFFAH12	151	160	170	180	190	200
		HHSNNGSLEK	DEVFVPPKKA	AVKWWVKYL-	NNPLGRILVL	TVQFILGWPL
FAH12	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLT	AATLLLGWPL
ATFAD2	151	HHSNTGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL
BNFAD2	151	HHSNTGSLER	DEVFVPR-RS	QTSSGTAST-	STTFGRVTML	TVQFTLGWPL
GMFAD2-1	151	HHSNTGSLDR	DEVFVPKPKS	KVAFWSKYL-	NNPLGRAVSL	LVTLTIGWPM
GMFAD2-2	151	HHSNTGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL
ZMFAD2	151	HHSNTGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL
RCFAD2	151	HHSNTGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTSLGWPL
		210	220	230	240	250
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFLYQ
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLS DAG	ILAVCFGLYR
BNFAD2	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP
GMFAD2-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR
GMFAD2-2	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAVVYGLFR
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK
RCFAD2	201	YLAFNVSGRP	YPR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ

FIG. 9A (CONT-2)

LFFAH12	251	260	270	280	290	300
FAH12	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLTFF	LQHTPSLPH	YDSTEWEWIR
ATFAD2	251	ATMAKGLAWV	MRIYGVPLLI	VNCFVLMITY	LQHTPAIPR	YGSSEWDWLR
BNFAD2	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTPSLPH	YDSSEWDWLR
GMFAD2-1	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTPSLPH	YDSSEWDWLR
GMFAD2-2	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTFALPH	YDSSEWDWLR
ZMFAD2	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITF	LQHTHPALPH	YTSSEWDWLR
RCFAD2	251	LAAAFGVWV	VRVYAVPLLI	VNAWLVLITY	LQHTPSLPH	YDSSEWDWLR
		LAIKGLAWV	VCVYGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR
LFFAH12	301	310	320	330	340	350
FAH12	301	GALVTVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG
ATFAD2	301	GAMVTVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG
BNFAD2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG
GMFAD2-1	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG
GMFAD2-2	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG
ZMFAD2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG
RCFAD2	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG
		GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG
		360	370	380	390	400
LFFAH12	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYNN	K-L.....
FAH12	351	EYYRYDGTFF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....
ATFAD2	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVYYNN	K-L.....
BNFAD2	351	EYYQFDGTPV	YKAMWREAKE	CIYVEPDROG	EKKGVFWYNN	KL*.....
GMFAD2-1	351	EYYQFDDTFF	YKALWREARE	CLYVEPDEGT	SEKGVWYRN	KY*.....
GMFAD2-2	351	EYYRFDETFF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....
ZMFAD2	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....

FIG. 9B

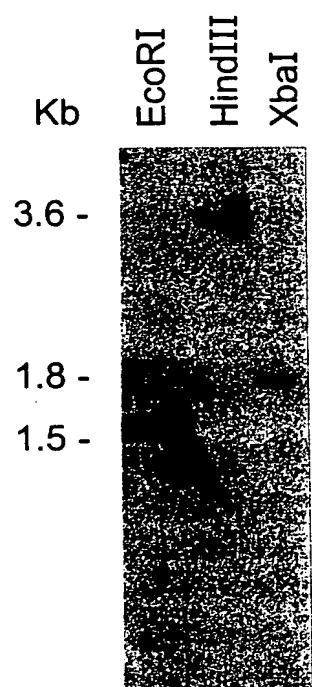


FIG. 10

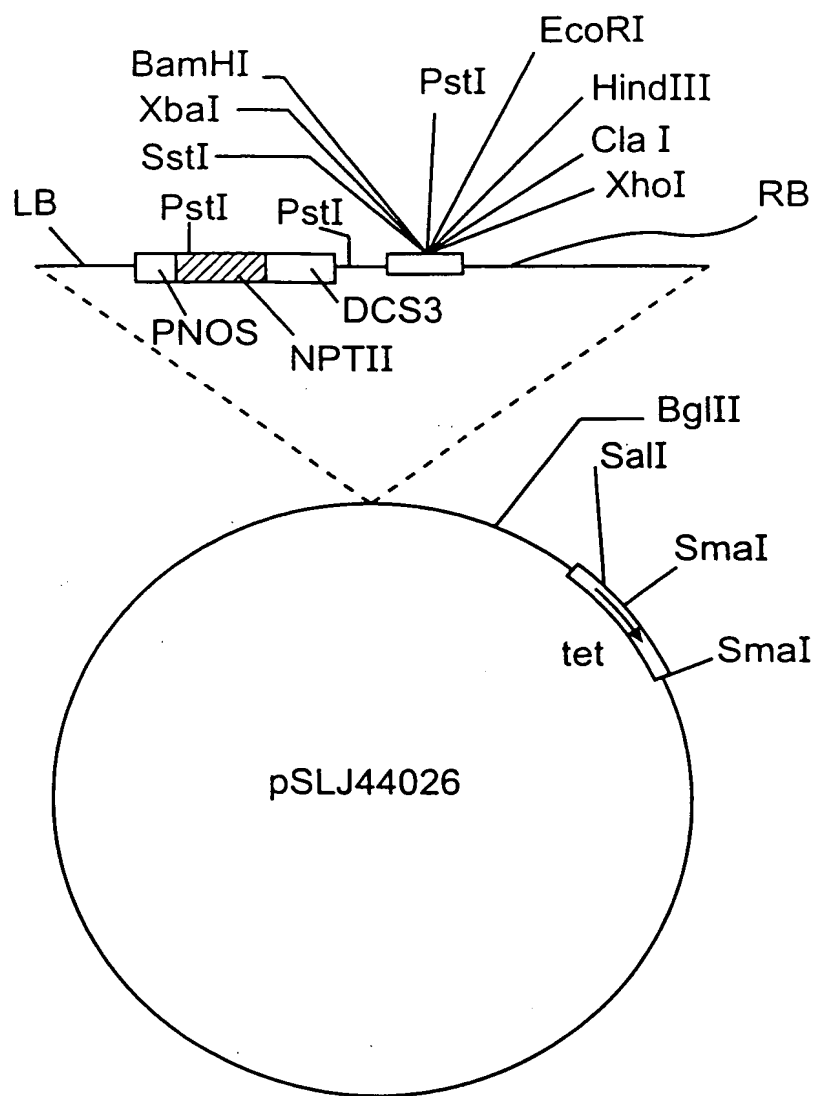


FIG. 11